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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/840,787

DATE: 06/15/2001  
TIME: 14:40:49

Input Set : N:\Crf3\RULE60\09840787.txt  
Output Set: N:\CRF3\06152001\I840787.raw

## SEQUENCE LISTING

- 3 (1) GENERAL INFORMATION:  
 5     (i) APPLICANT: Lal, Preeti  
 6                 Hillman, Jennifer L.  
 7                 Bandman, Olga  
 8                 Shah, Purvi  
 9                 Au-Young, Janice  
 10                Yue, Henry  
 11                Guegler, Karl J.  
 12                Corley, Neil C.  
 14     (ii) TITLE OF INVENTION: HUMAN REGULATORY MOLECULES  
 16     (iii) NUMBER OF SEQUENCES: 98  
 18     (iv) CORRESPONDENCE ADDRESS:  
 19         (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 20         (B) STREET: 3174 Porter Drive  
 21         (C) CITY: Palo Alto  
 22         (D) STATE: CA  
 23         (E) COUNTRY: USA  
 24         (F) ZIP: 94304  
 26     (v) COMPUTER READABLE FORM:  
 27         (A) MEDIUM TYPE: Diskette  
 28         (B) COMPUTER: IBM Compatible  
 29         (C) OPERATING SYSTEM: DOS  
 30         (D) SOFTWARE: FastSEQ for Windows Version 2.0  
 32     (vi) CURRENT APPLICATION DATA:  
 33         (A) APPLICATION NUMBER: US/09/840,787  
 34         (B) FILING DATE: 23-Apr-2001  
 35         (C) CLASSIFICATION:  
 37     (vii) PRIOR APPLICATION DATA:  
 38         (A) APPLICATION NUMBER: 09/518,865  
 39         (B) FILING DATE:  
 41     (viii) ATTORNEY/AGENT INFORMATION:  
 42         (A) NAME: Billings, Lucy J.  
 43         (B) REGISTRATION NUMBER: 36,749  
 44         (C) REFERENCE/DOCKET NUMBER: PF-0356 US  
 46     (ix) TELECOMMUNICATION INFORMATION:  
 47         (A) TELEPHONE: 415-855-0555  
 48         (B) TELEFAX: 415-845-4166  
 49         (C) TELEX:  
 52 (2) INFORMATION FOR SEQ ID NO: 1:  
 54     (i) SEQUENCE CHARACTERISTICS:  
 55         (A) LENGTH: 151 amino acids  
 56         (B) TYPE: amino acid  
 57         (C) STRANDEDNESS: single  
 58         (D) TOPOLOGY: linear  
 60     (vii) IMMEDIATE SOURCE:  
 61         (A) LIBRARY: U937NOT01

**ENTERED**

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62 (B) CLONE: 133  
 64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1 :  
 66 Met Thr Asn Glu Glu Pro Leu Pro Lys Lys Val Arg Leu Ser Glu  
 67 5 10 15  
 68 Thr Asp Phe Lys Val Met Ala Arg Asp Glu Leu Ile Leu Arg Trp  
 69 20 25 30  
 70 Lys Gln Tyr Glu Ala Tyr Val Gln Ala Leu Glu Gly Lys Tyr Thr  
 71 35 40 45  
 72 Asp Leu Asn Ser Asn Asp Val Thr Gly Leu Arg Glu Ser Glu Glu  
 73 50 55 60  
 74 Lys Leu Lys Gln Gln Gln Gln Glu Ser Ala Arg Arg Glu Asn Ile  
 75 65 70 75  
 76 Leu Val Met Arg Leu Ala Thr Lys Glu Gln Glu Met Gln Glu Cys  
 77 80 85 90  
 78 Thr Thr Gln Ile Gln Tyr Leu Lys Gln Val Gln Gln Pro Ser Val  
 79 95 100 105  
 80 Ala Gln Leu Arg Ser Thr Met Val Asp Pro Ala Ile Asn Leu Phe  
 81 110 115 120  
 82 Phe Leu Lys Met Lys Gly Glu Leu Glu Gln Thr Lys Asp Lys Leu  
 83 125 130 135  
 84 Glu Gln Ala Gln Asn Glu Leu Ser Ala Trp Lys Phe Thr Pro Asp  
 85 140 145 150

86 Arg

89 (2) INFORMATION FOR SEQ ID NO: 2:

91 (i) SEQUENCE CHARACTERISTICS:  
92 (A) LENGTH: 185 amino acids  
93 (B) TYPE: amino acid  
94 (C) STRANDEDNESS: single  
95 (D) TOPOLOGY: linear

97 (vii) IMMEDIATE SOURCE:

98 (A) LIBRARY: U937NOT01

99 (B) CLONE: 1762

101 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2 :

103	Met	Leu	Thr	Leu	Ala	Ser	Lys	Leu	Lys	Arg	Asp	Asp	Gly	Leu	Lys
104						5				10					15
105	Gly	Ser	Arg	Thr	Ala	Ala	Thr	Ala	Ser	Asp	Ser	Thr	Arg	Arg	Val
106						20				25					30
107	Ser	Val	Arg	Asp	Lys	Leu	Leu	Val	Lys	Glu	Val	Ala	Glu	Leu	Glu
108						35				40					45
109	Ala	Asn	Leu	Pro	Cys	Thr	Cys	Lys	Val	His	Phe	Pro	Asp	Pro	Asn
110						50				55					60
111	Lys	Leu	His	Cys	Phe	Gln	Leu	Thr	Val	Thr	Pro	Asp	Glu	Gly	Tyr
112						65				70					75
113	Tyr	Gln	Gly	Gly	Lys	Phe	Gln	Phe	Glu	Thr	Glu	Val	Pro	Asp	Ala
114						80				85					90
115	Tyr	Asn	Met	Val	Pro	Pro	Lys	Val	Lys	Cys	Leu	Thr	Lys	Ile	Trp
116						95				100					105
117	His	Pro	Asn	Ile	Thr	Glu	Thr	Gly	Glu	Ile	Cys	Leu	Ser	Leu	Leu
118						110				115					120

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119 Arg Glu His Ser Ile Asp Gly Thr Gly Trp Ala Pro Thr Arg Thr  
120 125 130 135  
121 Leu Lys Asp Val Val Trp Gly Leu Asn Ser Leu Phe Thr Asp Leu  
122 140 145 150  
123 Leu Asn Phe Asp Asp Pro Leu Asn Ile Glu Ala Ala Glu His His  
124 155 160 165  
125 Leu Arg Asp Lys Glu Asp Phe Arg Asn Lys Val Asp Asp Tyr Ile  
126 170 175 180  
127 Lys Arg Tyr Ala Arg  
128 185

131 (2) INFORMATION FOR SEQ ID NO: 3:

133 (i) SEQUENCE CHARACTERISTICS:  
134 (A) LENGTH: 59 amino acids  
135 (B) TYPE: amino acid  
136 (C) STRANDEDNESS: single  
137 (D) TOPOLOGY: linear

139 (vii) IMMEDIATE SOURCE:  
140 (A) LIBRARY: U937NOT01  
141 (B) CLONE: 1847

143 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3 :

145 Met Gly Lys Val Asn Val Ala Lys Leu Arg Tyr Met Ser Arg Asp  
146 5 10 15  
147 Asp Phe Arg Val Leu Thr Ala Val Glu Met Gly Met Lys Asn His  
148 20 25 30  
149 Glu Ile Val Pro Gly Ser Leu Ile Ala Ser Ile Ala Ser Leu Lys  
150 35 40 45  
151 His Gly Gly Cys Asn Lys Val Leu Arg Glu Leu Val Lys His  
152 50 55

155 (2) INFORMATION FOR SEQ ID NO: 4:

157 (i) SEQUENCE CHARACTERISTICS:  
158 (A) LENGTH: 338 amino acids  
159 (B) TYPE: amino acid  
160 (C) STRANDEDNESS: single  
161 (D) TOPOLOGY: linear

164 (vii) IMMEDIATE SOURCE:  
165 (A) LIBRARY: HMC1NOT01  
166 (B) CLONE: 9337

168 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4 :

170 Met Leu Glu Thr Phe Gly His Leu Val Ser Val Gly Trp Glu Thr  
171 5 10 15  
172 Thr Leu Glu Asn Lys Glu Leu Ala Pro Asn Ser Asp Ile Pro Glu  
173 20 25 30  
174 Glu Glu Pro Ala Pro Ser Leu Lys Val Gln Glu Ser Ser Arg Asp  
175 35 40 45  
176 Cys Ala Leu Ser Ser Thr Leu Glu Asp Thr Leu Gln Gly Gly Val  
177 50 55 60  
178 Gln Glu Val Gln Asp Thr Val Leu Lys Gln Met Glu Ser Ala Gln  
179 65 70 75  
180 Glu Lys Asp Leu Pro Gln Lys Lys His Phe Asp Asn Arg Glu Ser

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181	80	85	90
182	Gln Ala Asn Ser Gly Ala Leu Asp Thr Asn Gln Val Ser Leu Gln		
183	95	100	105
184	Lys Ile Asp Asn Pro Glu Ser Gln Ala Asn Ser Gly Ala Leu Asp		
185	110	115	120
186	Thr Asn Gln Val Leu Leu His Lys Ile Pro Pro Arg Lys Arg Leu		
187	125	130	135
188	Arg Lys Arg Asp Ser Gln Val Lys Ser Met Lys His Asn Ser Arg		
189	140	145	150
190	Val Lys Ile His Gln Lys Ser Cys Glu Arg Gln Lys Ala Lys Glu		
191	155	160	165
192	Gly Asn Gly Cys Arg Lys Thr Phe Ser Arg Ser Thr Lys Gln Ile		
193	170	175	180
194	Thr Phe Ile Arg Ile His Lys Gly Ser Gln Val Cys Arg Cys Ser		
195	185	190	195
196	Glu Cys Gly Lys Ile Phe Arg Asn Pro Arg Tyr Phe Ser Val His		
197	200	205	210
198	Lys Lys Ile His Thr Gly Glu Arg Pro Tyr Val Cys Gln Asp Cys		
199	215	220	225
200	Gly Lys Gly Phe Val Gln Ser Ser Ser Leu Thr Gln His Gln Arg		
201	230	235	240
202	Val His Ser Gly Glu Arg Pro Phe Glu Cys Gln Glu Cys Gly Arg		
203	245	250	255
204	Thr Phe Asn Asp Arg Ser Ala Ile Ser Gln His Leu Arg Thr His		
205	260	265	270
206	Thr Gly Ala Lys Pro Tyr Lys Cys Gln Asp Cys Gly Lys Ala Phe		
207	275	280	285
208	Arg Gln Ser Ser His Leu Ile Arg His Gln Arg Thr His Thr Gly		
209	290	295	300
210	Glu Arg Pro Tyr Ala Cys Asn Lys Cys Gly Lys Ala Phe Thr Gln		
211	305	310	315
212	Ser Ser His Leu Ile Gly His Gln Arg Thr His Asn Arg Thr Lys		
213	320	325	330
214	Arg Lys Lys Lys Gln Pro Thr Ser		
215	335		
218	(2) INFORMATION FOR SEQ ID NO: 5:		
220	(i) SEQUENCE CHARACTERISTICS:		
221	(A) LENGTH: 456 amino acids		
222	(B) TYPE: amino acid		
223	(C) STRANDEDNESS: single		
224	(D) TOPOLOGY: linear		
226	(vii) IMMEDIATE SOURCE:		
227	(A) LIBRARY: HMC1NOT01		
228	(B) CLONE: 9476		
230	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5 :		
232	Met Lys Ile Glu Glu Val Lys Ser Thr Thr Lys Thr Gln Arg Ile		
233	5	10	15
234	Ala Ser His Ser His Val Lys Gly Leu Gly Leu Asp Glu Ser Gly		
235	20	25	30

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236 Leu Ala Lys Gln Ala Ala Ser Gly Leu Val Gly Gln Glu Asn Ala  
237 35 40 45  
238 Arg Glu Ala Cys Gly Val Ile Val Glu Leu Ile Glu Ser Lys Lys  
239 50 55 60  
240 Met Ala Gly Arg Ala Val Leu Leu Ala Gly Pro Pro Gly Thr Gly  
241 65 70 75  
242 Lys Thr Ala Leu Ala Leu Ala Ile Ala Gln Glu Leu Gly Ser Lys  
243 80 85 90  
244 Val Pro Phe Cys Pro Met Val Gly Ser Glu Val Tyr Ser Thr Glu  
245 95 100 105  
246 Ile Lys Lys Thr Glu Val Leu Met Glu Asn Phe Arg Arg Ala Ile  
247 110 115 120  
248 Gly Leu Arg Ile Lys Glu Thr Lys Glu Val Tyr Glu Gly Glu Val  
249 125 130 135  
250 Thr Glu Leu Thr Pro Cys Glu Thr Glu Asn Pro Met Gly Gly Tyr  
251 140 145 150  
252 Gly Lys Thr Ile Ser His Val Ile Ile Gly Leu Lys Thr Ala Lys  
253 155 160 165  
254 Gly Thr Lys Gln Leu Lys Leu Asp Pro Ser Ile Phe Glu Ser Leu  
255 170 175 180  
256 Gln Lys Glu Arg Val Glu Ala Gly Asp Val Ile Tyr Ile Glu Ala  
257 185 190 195  
258 Asn Ser Gly Ala Val Lys Arg Gln Gly Arg Cys Asp Thr Tyr Ala  
259 200 205 210  
260 Thr Glu Phe Asp Leu Glu Ala Glu Glu Tyr Val Pro Leu Pro Lys  
261 215 220 225  
262 Gly Asp Val His Lys Lys Glu Ile Ile Gln Asp Val Thr Leu  
263 230 235 240  
264 His Asp Leu Asp Val Ala Asn Ala Arg Pro Gln Gly Gly Gln Asp  
265 245 250 255  
266 Ile Leu Ser Met Met Gly Gln Leu Met Lys Pro Lys Lys Thr Glu  
267 260 265 270  
268 Ile Thr Asp Lys Leu Arg Gly Glu Ile Asn Lys Val Val Asn Lys  
269 275 280 285  
270 Tyr Ile Asp Gln Gly Ile Ala Glu Leu Val Pro Gly Val Leu Phe  
271 290 295 300  
272 Val Asp Glu Val His Met Leu Asp Ile Glu Cys Phe Thr Tyr Leu  
273 305 310 315  
275 His Arg Ala Leu Glu Ser Ser Ile Ala Pro Ile Val Ile Phe Ala  
276 320 325 330  
277 Ser Asn Arg Gly Asn Cys Val Ile Arg Gly Thr Glu Asp Ile Thr  
278 335 340 345  
279 Ser Pro His Gly Ile Pro Leu Asp Leu Leu Asp Arg Val Met Ile  
280 350 355 360  
281 Ile Arg Thr Met Leu Tyr Thr Pro Gln Glu Met Lys Gln Ile Ile  
282 365 370 375  
283 Lys Ile Arg Ala Gln Thr Glu Gly Ile Asn Ile Ser Glu Glu Ala  
284 380 385 390  
285 Leu Asn His Leu Gly Glu Ile Gly Thr Lys Thr Thr Leu Arg Tyr

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/840,787

DATE: 06/15/2001  
TIME: 14:40:50

Input Set : N:\Crf3\RULE60\09840787.txt  
Output Set: N:\CRF3\06152001\I840787.raw

L:33 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:34 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:1081 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:1083 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:1085 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:1426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24